

O'Bryen, Barbara

From: Switzer, Juliet
Sent: Friday, December 17, 2004 2:37 PM
To: O'Bryen, Barbara
Subject: FW: search request

see below.

please search in all nucleic acid prior art databases and return results on disk.
thanks.

-----Original Message-----

From: Spencer, Mark
Sent: Friday, December 17, 2004 2:36 PM
To: Switzer, Juliet
Subject: RE: search request

Juliet,

Send a search request to the STIC biotech with a note to the searcher to contact me to get the CD. I will give the searcher the CD and they will copy and paste the sequence into their search system.

Thanks,
Mark

-----Original Message-----

From: Switzer, Juliet
Sent: Friday, December 17, 2004 2:29 PM
To: Spencer, Mark
Subject: search request

hi mark,

I need a search of seq id no 1 of 09/925065. The CRFE in the case says to contact you because the sequence listing is not in the database.

thanks.

Juliet

RESULT 1

AB045146

LOCUS AB045146 27870 bp DNA linear PRI 22-AUG-2000

DEFINITION Homo sapiens TPMT gene for thiopurine S-methyltransferase, complete cds.

ACCESSION AB045146

VERSION AB045146.1 GI:8777468

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nakamura, Y.

TITLE Genomic structure of Thiopurine S-methyltransferase gene

JOURNAL Published Only in DataBase (2000)

REFERENCE 2 (bases 1 to 27870)

AUTHORS Nakamura, Y.

TITLE Direct Submission

JOURNAL Submitted (23-JUN-2000) Yusuke Nakamura, Human Genome Center, Institute of Medical Science, The University of Tokyo, Laboratory of Molecular Medicine, Shirokanedai 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:kumikok@ims.u-tokyo.ac.jp, Tel:81-03-5449-5375, Fax:81-03-5449-5406)

FEATURES Location/Qualifiers

source 1. 27870
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6p22.3"
 /country="Japan"

gene join(6816..6955,8033..8125,12221..12353,16234..16286,
 16914..16988,22064..22149,23779..23823,25177..25289)
 /gene="TPMT"

CDS join(6816..6955,8033..8125,12221..12353,16234..16286,
 16914..16988,22064..22149,23779..23823,25177..25289)
 /gene="TPMT"
 /codon_start=1
 /product="thiopurine S-methyltransferase"
 /protein_id="BAA97037.1"
 /db_xref="GI:8777469"
 /translation="MDGTRTSLDIEEYSDTEVQKNQVLTLEEWQDKWVNGKTAFHQEKGQLLKKHLDLKGKSLRVFFPLCGKAVEMKWFADRGHSVVGVEISELGIQEFTEQNLSYSEEPITEIPGTVKFKSSSGNISLYCCSIFDLPRTRNIGKFDIMIWDRGALVAINPGDRKCYADTMFSLLGKKFQYLLCVLSYDPTKHPGPPFYVPHAEIERLFGKICNIRCLEKVDAFEERHKSWGIDCLFEKLYLLTEK"

ORIGIN

Query Match 99.5%; Score 437.6; DB 9; Length 27870;
 Best Local Similarity 98.6%; Pred. No. 5.6e-83;
 Matches 434; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGAGAGTGTAGTGAGCCAAGATTGTGCCCTGCACTCCAGCGTGGTAACAGAGTGAGA 60
 ||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 24093 CARARAGTGTAGTKAGCCAARATTGTGCCMCTGCACTCCAGCGTGGTAACAGAGTGAGA 24152

Qy 61 CTCCATCTAAAAAAAAACCTATTGTGAACTATTAGTATATTAGTATCTAGAGTATGT 120

Db 24153 |||||||CTCCATCTAAAAAAAAACCTATTGTGAACCTATTAGTATATTAGTATCTAGAGTATGT 24212

Qy 121 CTATAAAATTAAAAGATAAAGACCATTATTGAAAGTTGTTATCTTAGAAAAGGAA 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 24213 CTATAAAATTAAAAGATAAAGACCATTATTGAAAGTTGTTATCTTAGAAAAGGAA 24272

Qy 181 CTAATCTCTGAAATATGCTCTGTRTATGCTATGCTCTATGTTAAAGGTATTGAA 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 24273 CTAATCTCTGAAATATGCTCTGTTATGCTATGCTCTATGTTAAAGGTATTGAA 24332

Qy 241 CTTTCTAGAGAGATGGTATATATTTTTATTGTTATTTGAGATAGGATCTTGAT 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 24333 CTTTCTAGAGAGATGGTATATATTTTTATTGTTATTTGAGATAGGATCTTGAT 24392

Qy 301 CTGTCACCCAGGCTGGAGTACAGAAGTGCAATCACAGCTCACTGCAGCCTCGACCTCCCT 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 24393 CTGTCACCCAGGCTGGAGTACAGAAGTGCAATCACAGCTCACTGCAGCCTCGACCTCCCT 24452

Qy 361 GGGCACAAGTGATCCTCCCACCTCAGCCTCCCAAGTTCTGGGACCAGAGGCATGCACCA 420
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 24453 GGGCACAAGTGATCCTCCCACCTCAGCCTCCCAAGTTCTGGGACCAGAGGCATGCACCA 24512

Qy 421 CAATGCTTAGCTAATTTTC 440
|||:|||||:|||||:|||||:|||||

Db 24513 CAATGCTTAGCTAATTTTC 24532

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 03:59:11 ; Search time 3313 Seconds
(without alignments)
6280.552 Million cell updates/sec

Title: US-09-925065A-SEQ1

Perfect score: 440

Sequence: 1 cagagagtgttagtgagccaa.....caatgcttagctaattttc 440

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	
	No.	Score	Match	Length	DB ID	Description
	1	437.6	99.5	27870	9 AB045146	AB045146 Homo sapi
c	2	436.4	99.2	147927	9 AL589723	AL589723 Human DNA
	3	359.6	81.7	170346	2 AC145821	AC145821 Papio anu
	4	159.8	36.3	185353	9 AL162732	AL162732 Human DNA

C	5	153.4	34.9	164310	2	AC016156	AC016156	Homo sapi
C	6	153.4	34.9	205834	9	AP006193	AP006193	Homo sapi
	7	151	34.3	198410	2	AP000831	AP000831	Homo sapi
	8	148.6	33.8	181086	9	AL133215	AL133215	Human DNA
	9	148.6	33.8	215103	2	AC058821	AC058821	Homo sapi
	10	148.2	33.7	203230	2	AC026346	AC026346	Homo sapi
	11	148	33.6	149374	2	AC053520	AC053520	Homo sapi
	12	148	33.6	175754	9	AC084018	AC084018	Homo sapi
C	13	147.8	33.6	44024	9	AC133963	AC133963	Homo sapi
	14	147.4	33.5	33026	9	AF156673	AF156673	Homo sapi
	15	147.4	33.5	177893	9	AC005089	AC005089	Homo sapi
	16	147	33.4	179262	9	AL355343	AL355343	Human DNA
C	17	147	33.4	184778	2	AC023567	AC023567	Homo sapi
	18	146.4	33.3	108893	9	AC079169	AC079169	Homo sapi
	19	146.2	33.2	184515	9	AC010653	AC010653	Homo sapi
C	20	146	33.2	179155	9	AL353748	AL353748	Human DNA
C	21	145.2	33.0	181466	2	AC137089	AC137089	Homo sapi
C	22	145	33.0	87507	9	AC132006	AC132006	Homo sapi
	23	145	33.0	148260	2	AC068498	AC068498	Homo sapi
	24	144.8	32.9	171364	9	AL359844	AL359844	Human DNA
	25	144.6	32.9	153803	2	AC055722	AC055722	Homo sapi
	26	144.4	32.8	182078	2	AC140904	AC140904	Homo sapi
C	27	143	32.5	78816	2	AC145755	AC145755	Pan trogl
C	28	143	32.5	201659	2	AC146419	AC146419	Pan trogl
	29	142.6	32.4	131329	9	AC004873	AC004873	Homo sapi
C	30	142.6	32.4	156630	9	BS000087	BS000087	Pan trogl
C	31	142.6	32.4	157435	9	HS50024	AL034380	Human DNA
C	32	142.6	32.4	163914	9	AC098487	AC098487	Homo sapi
	33	142.6	32.4	189319	9	AL158154	AL158154	Human DNA
C	34	142.6	32.4	315681	2	AL355380	AL355380	Homo sapi
C	35	142.4	32.4	198333	9	BS000088	BS000088	Pan trogl
C	36	142.2	32.3	99701	9	AC109319	AC109319	Homo sapi
C	37	142.2	32.3	103097	9	AL445464	AL445464	Human DNA
C	38	142.2	32.3	118484	9	AY268350	AY268350	Homo sapi
C	39	142.2	32.3	135162	9	HS451B21	AL033522	Human DNA
	40	142.2	32.3	143614	2	AC025147	AC025147	Homo sapi
	41	142.2	32.3	158500	2	AL359206	AL359206	Homo sapi
	42	142.2	32.3	161678	2	AC009337	AC009337	Homo sapi
	43	142.2	32.3	175132	9	AC008134	AC008134	Homo sapi
	44	142.2	32.3	178328	2	AC019265	AC019265	Homo sapi
	45	142.2	32.3	179375	2	AC092971	AC092971	Homo sapi

Run on: December 22, 2004, 03:59:06 ; Search time 407 Seconds
(without alignments)
5675.050 Million cell updates/sec

Title: US-09-925065A-SEQ1
Perfect score: 440
Sequence: 1 cagagagtgttagtgagccaa.....caatgcttagctaattttc 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	%
<hr/>							
c 1	137	31.1	98865	6	ABQ78054	Abq78054 Human Ras	
	2	136.2	31.0	114693	8	AAD48308	Aad48308 Human tra
	3	133.8	30.4	10515	6	ABK10772	Abk10772 Human sma
	4	133	30.2	118384	10	ABX56555	Abx56555 Human aut
c 5	132.4	30.1	46340	3	ABN97978	Abn97978 Human ret	
c 6	131.4	29.9	190117	10	ADL13780	Adl13780 Osteoarth	
c 7	131	29.8	52216	4	AAH28355	Aah28355 Nucleotid	
c 8	131	29.8	52216	6	ABL50307	Ab150307 Human mus	
	9	130.8	29.7	190117	10	ADL13780	Adl13780 Osteoarth
10	130.2	29.6	110000	5	AAF84800	Aaf84800 Nucleotid	
11	129.8	29.5	49806	9	ADB16927	Adb16927 Human DYX	
12	129.6	29.5	22013	4	AAK85635	Aak85635 Human imm	

13	129.6	29.5	22013	5	ABA16084	Aba16084 Human ner	
14	129.6	29.5	22026	4	AAK85636	Aak85636 Human imm	
15	129.6	29.5	22026	5	ABA16085	Aba16085 Human ner	
16	129.6	29.5	175737	6	ABK83571	Abk83571 Human cDN	
17	129.6	29.5	175737	10	ADL13596	Adl13596 Osteoarth	
18	129.6	29.5	175737	12	ADQ18934	Adq18934 Human sof	
c	19	129.4	29.4	119950	2	AAX90201	Aax90201 Human yes
	20	128.6	29.2	52216	4	AAH28355	Aah28355 Nucleotid
	21	128.6	29.2	52216	6	ABL50307	Abl50307 Human mus
c	22	128.4	29.2	96593	11	ADL27146	Adl27146 Human gen
c	23	128.4	29.2	96595	9	ADA03068	Ada03068 Human PPP
c	24	128.4	29.2	96595	10	ADB72806	Adb72806 Human PPP
c	25	128.4	29.2	96596	9	ADA66352	Ada66352 Human PPP
	26	127.8	29.0	17335	4	ABK42393	Abk42393 Genomic s
	27	127.8	29.0	17335	9	ADB60549	Adb60549 Connectiv
	28	127.8	29.0	19882	4	ABK42394	Abk42394 Genomic s
	29	127.8	29.0	19882	9	ADB60550	Adb60550 Connectiv
	30	127.8	29.0	86765	10	ADD14752	Add14752 Human src
c	31	127.4	29.0	12392	5	ABA15896	Aba15896 Human ner
c	32	127.4	29.0	166181	12	ADQ20461	Adq20461 Human sof
c	33	127.4	29.0	166181	12	ADQ18633	Adq18633 Human sof
	34	127	28.9	176001	12	ADK43203	Adk43203 Human pro
	35	127	28.9	186739	12	ADK43195	Adk43195 Human pro
	36	126.8	28.8	7385	4	AAH72843	Aah72843 Human cer
c	37	126.4	28.7	94719	10	ADE95902	Ade95902 Human STA
c	38	126.4	28.7	94720	9	ADA02654	Ada02654 Human STA
c	39	126.4	28.7	94720	10	ADB72392	Adb72392 Human STA
	40	126	28.6	8855	5	ABA19146	Aba19146 Human ner
	41	126	28.6	51474	5	AAF97846	Aaf97846 Human neu
c	42	125.8	28.6	57296	4	AAK78847	Aak78847 Human imm
c	43	125.8	28.6	57296	4	AAK78170	Aak78170 Human imm
c	44	125.8	28.6	57296	4	AAK79364	Aak79364 Human imm
c	45	125.8	28.6	57296	4	AAK86799	Aak86799 Human imm

Run on: December 22, 2004, 04:17:56 ; Search time 93 Seconds
(without alignments)
3362.872 Million cell updates/sec

Title: US-09-925065A-SEQ1
Perfect score: 440
Sequence: 1 cagagagtgttagtgagccaa.....caatgcttagctaattttc 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	Description
<hr/>							
c 1	125.8	28.6	319608	4	US-09-539-333D-1	Sequence 1, Appli	
c 2	125.8	28.6	319608	4	US-09-679-409-1	Sequence 1, Appli	
c 3	123.4	28.0	44848	4	US-09-435-739-42	Sequence 42, Appli	
c 4	123.4	28.0	44848	4	US-09-988-113-42	Sequence 42, Appli	
c 5	123.2	28.0	246240	2	US-08-724-394A-20	Sequence 20, Appli	
c 6	123.2	28.0	246240	2	US-08-724-394A-21	Sequence 21, Appli	
c 7	123.2	28.0	246240	2	US-08-724-394A-22	Sequence 22, Appli	
c 8	120.2	27.3	54550	4	US-10-327-189-42	Sequence 42, Appli	
c 9	117.6	26.7	12597	4	US-09-705-299-12	Sequence 12, Appli	
c 10	117.6	26.7	30350	4	US-10-118-328-3	Sequence 3, Appli	
c 11	117.2	26.6	29629	4	US-09-729-995-3	Sequence 3, Appli	
c 12	117.2	26.6	29629	4	US-10-135-689-3	Sequence 3, Appli	
c 13	116.8	26.5	90541	4	US-09-759-359A-3	Sequence 3, Appli	
c 14	116.8	26.5	90541	4	US-10-207-973-3	Sequence 3, Appli	
c 15	116.6	26.5	33769	4	US-09-544-398B-8	Sequence 8, Appli	
c 16	116.6	26.5	33769	4	US-09-543-771-8	Sequence 8, Appli	
c 17	116.2	26.4	246240	2	US-08-724-394A-20	Sequence 20, Appli	
c 18	116.2	26.4	246240	2	US-08-724-394A-21	Sequence 21, Appli	

c	19	116.2	26.4	246240	2	US-08-724-394A-22	Sequence 22, Appl
	20	115.6	26.3	307	4	US-09-513-999C-29011	Sequence 29011, A
	21	114.8	26.1	6678	3	US-08-816-617A-1	Sequence 1, Appli
c	22	114.8	26.1	98844	4	US-09-791-211-10	Sequence 10, Appl
	23	114.6	26.0	75395	4	US-09-984-890-3	Sequence 3, Appli
	24	114.6	26.0	75395	4	US-10-274-194-3	Sequence 3, Appli
	25	114	25.9	64467	4	US-09-803-671B-3	Sequence 3, Appli
c	26	113.6	25.8	54945	4	US-09-967-669-10	Sequence 10, Appl
	27	113	25.7	46718	4	US-09-816-093-3	Sequence 3, Appli
c	28	112.2	25.5	53332	4	US-09-801-861-3	Sequence 3, Appli
c	29	112.2	25.5	53332	4	US-10-224-562-3	Sequence 3, Appli
	30	112.2	25.5	70000	4	US-09-851-896-3	Sequence 3, Appli
c	31	111.6	25.4	30350	4	US-10-118-328-3	Sequence 3, Appli
c	32	111.6	25.4	43950	3	US-09-735-934A-3	Sequence 3, Appli
c	33	111.6	25.4	43950	4	US-10-060-332-3	Sequence 3, Appli
c	34	111.6	25.4	43950	4	US-10-339-657-3	Sequence 3, Appli
c	35	111.6	25.4	64467	4	US-09-803-671B-3	Sequence 3, Appli
	36	111.2	25.3	13158	2	US-08-687-080-105	Sequence 105, App
c	37	111.2	25.3	55298	4	US-09-491-356C-1	Sequence 1, Appli
	38	110.6	25.1	63000	4	US-09-780-172-18	Sequence 18, Appli
c	39	110.6	25.1	116592	4	US-09-818-512-3	Sequence 3, Appli
c	40	110.4	25.1	619	4	US-09-152-060-17	Sequence 17, Appli
	41	110.4	25.1	84495	3	US-09-797-906-3	Sequence 3, Appli
	42	109.8	25.0	29485	4	US-09-785-381-6	Sequence 6, Appli
	43	109.8	25.0	55298	4	US-09-491-356C-1	Sequence 1, Appli
c	44	109.8	25.0	81001	4	US-09-750-580-1	Sequence 1, Appli
	45	109.8	25.0	107820	4	US-09-792-616-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 04:18:16 ; Search time 4686 Seconds
(without alignments)
518.389 Million cell updates/sec

Title: US-09-925065A-SEQ1

Perfect score: 440

Sequence: 1 cagagagtgtagtgagccaa.....caatgcttagctaattttc 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result

Query

No.	Score	Match	Length	DB	ID	Description
C 1	152.4	34.6	667	13	US-10-027-632-19561	Sequence 19561, A
C 2	152.4	34.6	667	15	US-10-027-632-19561	Sequence 19561, A
C 3	140.2	31.9	2393	13	US-10-027-632-102715	Sequence 102715,
C 4	140.2	31.9	2393	15	US-10-027-632-102715	Sequence 102715,
C 5	140.2	31.9	2394	13	US-10-027-632-111593	Sequence 111593,
C 6	140.2	31.9	2394	13	US-10-027-632-111594	Sequence 111594,
C 7	140.2	31.9	2394	15	US-10-027-632-111593	Sequence 111593,
C 8	140.2	31.9	2394	15	US-10-027-632-111594	Sequence 111594,
C 9	137	31.1	98865	9	US-09-770-689A-3	Sequence 3, Appli
10	136.2	31.0	114693	18	US-10-473-392-3	Sequence 3, Appli
C 11	132.8	30.2	430442	18	US-10-417-375-128	Sequence 128, App
C 12	132.6	30.1	52745	17	US-10-741-601-5726	Sequence 5726, Ap
13	132.4	30.1	161334	13	US-10-087-192-730	Sequence 730, App
C 14	132.2	30.0	1011	13	US-10-027-632-253775	Sequence 253775,
C 15	132.2	30.0	1011	15	US-10-027-632-253775	Sequence 253775,
C 16	131	29.8	52216	9	US-09-747-810-1	Sequence 1, Appli
17	129.8	29.5	50000	15	US-10-364-505-7	Sequence 7, Appli
18	129.8	29.5	50000	17	US-10-681-199-7	Sequence 7, Appli
C 19	128.8	29.3	104062	13	US-10-087-192-916	Sequence 916, App
C 20	128.6	29.2	43173	13	US-10-087-192-2026	Sequence 2026, Ap
21	128.6	29.2	52216	9	US-09-747-810-1	Sequence 1, Appli
C 22	128.4	29.2	96595	15	US-10-034-650-34	Sequence 34, Appl
23	127.8	29.0	17335	9	US-09-764-847-1280	Sequence 1280, Ap
24	127.8	29.0	17335	14	US-10-092-154-1280	Sequence 1280, Ap
25	127.8	29.0	19882	9	US-09-764-847-1281	Sequence 1281, Ap
26	127.8	29.0	19882	14	US-10-092-154-1281	Sequence 1281, Ap
27	127	28.9	176001	16	US-10-210-556-27	Sequence 27, Appl
28	127	28.9	186739	16	US-10-210-556-19	Sequence 19, Appl
C 29	126.4	28.7	94720	16	US-10-052-482-160	Sequence 160, App
C 30	125.8	28.6	160921	13	US-10-087-192-1672	Sequence 1672, Ap
C 31	125.8	28.6	319608	15	US-10-147-603-1	GENERAL INFORMATI
C 32	125.2	28.5	21739	17	US-10-741-601-5713	Sequence 5713, Ap
33	125.2	28.5	37940	15	US-10-348-073A-12	Sequence 12, Appl
34	125.2	28.5	38000	15	US-10-175-627-11	Sequence 11, Appl
C 35	125	28.4	50000	15	US-10-364-505-7	Sequence 7, Appli
C 36	125	28.4	50000	17	US-10-681-199-7	Sequence 7, Appli
C 37	124.8	28.4	46130	15	US-10-017-161-985	Sequence 985, App
38	124.8	28.4	55611	15	US-10-017-161-783	Sequence 783, App
39	124.6	28.3	24446	17	US-10-741-601-5740	Sequence 5740, Ap
C 40	124.6	28.3	389182	13	US-10-087-192-1102	Sequence 1102, Ap
41	124.4	28.3	21913	10	US-09-764-891-6065	Sequence 6065, Ap
42	124.4	28.3	21913	10	US-09-764-891-6066	Sequence 6066, Ap
43	124.4	28.3	21913	10	US-09-764-891-6067	Sequence 6067, Ap
C 44	124.4	28.3	54000	10	US-09-843-377-11	Sequence 11, Appl
C 45	124.4	28.3	54000	17	US-10-819-244-11	Sequence 11, Appl

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 04:16:31 ; Search time 2965 Seconds
(without alignments)
5407.582 Million cell updates/sec

Title: US-09-925065A-SEQ1

Perfect score: 440

Sequence: 1 cagagagtgtagtgagccaa.....caatgcttagctaattttc 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
c 1	136.6	31.0	596	7	CN274384	CN274384 170006000
c 2	135.2	30.7	660	8	AQ013712	AQ013712 RPCI11-23
3	133	30.2	3868	3	BC033908	BC033908 Homo sapi
c 4	132.2	30.0	582	6	CD696556	CD696556 EST13079
5	131.8	30.0	571	4	BM826251	BM826251 K-EST0098
6	130.2	29.6	553	5	BQ100951	BQ100951 ij22b01.y
c 7	130.2	29.6	557	7	CK819114	CK819114 if08b12.x
8	130.2	29.6	560	4	BM128002	BM128002 if08b12.y
c 9	130.2	29.6	563	4	BM127735	BM127735 if08b12.x

10	130.2	29.6	565	7	CK819115	CK819115 if08b12.y
c 11	130.2	29.6	566	5	BQ102328	BQ102328 ij20b06.x
12	130.2	29.6	573	5	BQ086237	BQ086237 ij20b06.y
13	130.2	29.6	592	7	CK823027	CK823027 ij22b01.y
c 14	130.2	29.6	616	5	BQ004314	BQ004314 UI-H-EI0-
15	130.2	29.6	645	6	CB128065	CB128065 K-EST0177
16	130.2	29.6	676	4	BI828537	BI828537 603078424
c 17	128.6	29.2	562	7	CK823026	CK823026 ij22b01.x
c 18	128.4	29.2	534	8	B86133	B86133 RPCI11-22C1
c 19	127.2	28.9	444	4	BI481343	BI481343 H2RPE-163
20	127.2	28.9	651	5	BX488111	BX488111 DKFZp686E
c 21	126.6	28.8	666	9	AG073023	AG073023 Pan trogl
22	125.4	28.5	6146	8	AQ839831	AQ839831 260L13-C4
c 23	123.4	28.0	666	9	AG167441	AG167441 Pan trogl
c 24	123.2	28.0	513	2	AW973217	AW973217 EST385315
c 25	123.2	28.0	660	8	BZ603692	BZ603692 WHADP18TR
c 26	123.2	28.0	1003	4	BM542339	BM542339 AGENCOURT
27	123	28.0	565	1	AA577885	AA577885 nn25d10.s
28	122.8	27.9	351	1	AI014347	AI014347 am51g08.s
c 29	122.8	27.9	515	5	BX479862	BX479862 DKFZp686P
30	122.8	27.9	656	5	BU681280	BU681280 UI-CF-EC1
c 31	122.2	27.8	309	1	AA533823	AA533823 nj94b10.s
32	122	27.7	688	6	CA426034	CA426034 UI-H-DF0-
33	122	27.7	699	4	BI871115	BI871115 603394292
c 34	122	27.7	706	9	AG121314	AG121314 Pan trogl
35	122	27.7	780	7	CN431118	CN431118 170005999
c 36	122	27.7	1281	3	AF130056	AF130056 Homo sapi
37	121.8	27.7	443	1	AI278802	AI278802 qo42d10.x
c 38	121.6	27.6	379	1	AA179163	AA179163 zp12d02.s
39	121.6	27.6	476	8	AQ735338	AQ735338 HS_3024_B
c 40	121.2	27.5	770	5	BX953657	BX953657 DKFZp781O
41	120.8	27.5	390	8	B03790	B03790 cSRSL-187d7-
c 42	120.6	27.4	670	9	AG056372	AG056372 Pan trogl
c 43	120.4	27.4	356	2	AW834135	AW834135 MR2-TT001
c 44	120.4	27.4	356	2	AW834160	AW834160 MR2-TT001
45	120.4	27.4	479	5	BX089489	BX089489 BX089489